

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: January 16, 2003, 15:20.22, Search time 63.8603 Seconds

(Without alignments)
14944.909 Million cell updates/sec

Title: US-09-026 459a 36

Perfect score: 3113
Sequence: 1 GCCGTCATCTCAGACTCTT . . . AATGACATATTGATGACT 3113

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3105.4	99.8	3232	1 US-08-038-760-2	Sequence 2, Appl
3	3105.4	99.8	3232	1 US-08-470-091-1	Sequence 1, Appl
4	3105.4	99.8	3232	1 US-08-470-091-2	Sequence 2, Appl
5	2415	77.6	2994	1 US-08-204-329-2	Sequence 2, Appl
6	2415	77.6	2994	1 US-08-482-627-4	Sequence 4, Appl
7	2415	77.6	2994	1 US-08-801-092-3	Sequence 3, Appl
8	2415	77.6	2994	1 US-08-801-092-3	Sequence 3, Appl
9	2413.4	77.5	2994	1 US-08-315-113-3	Sequence 3, Appl
10	2413.4	77.5	2994	1 US-08-315-113-3	Sequence 3, Appl
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12	68.8	2.2	2808	1 US-07-708-962-1	Sequence 1, Appl
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18	59	1.9	7218	1 US-08-232-463-14	Sequence 1, Appl
19	51	1.6	3747	1 US-09-213-293D-2	Sequence 2, Appl
20	44.6	1.4	1803	4 US-09-134-001C-799	Sequence 799, App
21	44.6	1.4	15363	4 US-08-961-527-139	Sequence 139, App
22	44.4	1.4	20674	2 US-09-641-638-651	Sequence 651, App
23	44.4	1.4	19124	2 US-08-487-826B-13	Sequence 13, Appl
24	43.8	1.4	1056	4 US-09-134-001C-1550	Sequence 1550, App
25	43.2	1.4	509	4 US-09-030-607-202	Sequence 202, App
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27	43.2	1.4	509	4 US-09-439-313-202	Sequence 202, App

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29	43.2	1.4	509	4 US-09-352-615A-292	Sequence 292, App
30	43	1.4	6852	1 US-07-867-106-2	Sequence 2, Appl
31	42.8	1.4	615	4 US-08-998-416-186	Sequence 186, App
32	42.6	1.4	1189	1 US-08-307-591-2	Sequence 2, Appl
33	42.6	1.4	2606	4 US-09-234-827B-3	Sequence 3, Appl
34	42.4	1.4	1186	2 US-08-731-722-5	Sequence 5, Appl
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36	42	1.3	1864	4 US-09-468-265-4	Sequence 4, Appl
37	41.8	1.3	1679	4 US-09-308-060-1	Sequence 1, Appl
38	41.4	1.3	10124	2 US-08-487-826B-13	Sequence 13, Appl
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42	40.6	1.3	860	4 US-08-960-022-3	Sequence 287, App
43	40.6	1.3	4078	2 US-09-129-112-3	Sequence 3, Appl
44	40.6	1.3	6265	4 US-09-129-112-3	Sequence 3, Appl
45	40.6	1.3	12124	1 US-08-181-271A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1
US-08-038-760-1
Sequence 1, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
METHOD OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1 0, Version #1 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038-760
FILING DATE: 19930325
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Polissand, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 669-9741/6864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19 2469
US-08-038-760-1
Query Match 99.8% Score 3105.4; DB 1; Length 3232;
Rest local Similarity 100.0%; Pred. No. 0;
Matches 3106; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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 DB 184 ACATGGAAGCTATATATTTGACACAGCCGACCTGGATATTTAGTGAATTAATCTG 244
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 DB 304 ATGGAAGATGATCTGCTGATTTTCAATTCATTAATCTGATGCTGATATTTAT 363
 QY 247 AAAGCTCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 306
 DB 364 AAAGCTCTGCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 423
 QY 307 GATTGATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 366
 DB 424 GATTGATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 483
 QY 367 GAAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 426
 DB 484 GAAATGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 543
 QY 427 GTGAAAAATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 486
 DB 544 GTGAAAAATGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTAT 603
 QY 487 TCTATGATCTGCTGAGAGTTGAAATCTTTTAAAGATGCTGAAATTTATTTATTTAT 546
 DB 604 TCTATGATCTGCTGAGAGTTGAAATCTTTTAAAGATGCTGAAATTTATTTATTTAT 663
 QY 547 AATAAGATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 606
 DB 664 AATAAGATCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 723
 QY 607 ATAGACATTTTGAACACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 666
 DB 724 ATAGACATTTTGAACACAGACAGACAGACAGACAGACAGACAGACAGACAGACAG 783
 QY 667 GATATCTGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 726
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 QY 727 ATTTAAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 786
 DB 844 ATTTAAATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 903
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 QY 847 GAGAAATTTGCTAAAGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 906
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 QY 907 CTGAGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 966
 DB 1024 CTGAGATCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
 QY 967 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1026
 DB 1084 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1143
 QY 1027 GCGTGGCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1086
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 QY 1147 TTTTCAAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1206
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 QY 1207 AAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1266
 DB 1324 AAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1383
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 DB 1504 TTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1563
 QY 1447 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1506
 DB 1564 GAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
 QY 1507 TTAGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1566
 DB 1624 TTAGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
 QY 1567 GCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1626
 DB 1684 GCGCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1743
 QY 1627 GTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1686
 DB 1744 GTGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1803
 QY 1687 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1746
 DB 1804 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1863
 QY 1747 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1806
 DB 1864 TATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1923
 QY 1807 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
 DB 1924 GAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
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 DB 1984 ATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
 QY 1927 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1986
 DB 2044 AGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2103
 QY 1987 CCGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2046
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 QY 2047 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2106
 DB 2164 AGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2223
 QY 2107 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2166
 DB 2224 ATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2283
 QY 2167 CCGCTGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2226

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Db 2284 CCTCTAAACGACTGAAAAACGCTTGTGATTTAGGAGTCAGATGAGGAGGAGTGA 2343
QY 2227 AGTAAACATCTCCAGAGAGTCCAAATTTTCAGCAAAATGGCGAAGATGACTTACT 2286
Db 2344 AGTAAACATCTCCAGAGAGTCCAAATTTTCAGCAAAATGGCGAAGATGACTTACT 2493
QY 2287 CGAACGAGATGCAAAAGCAGAAATGATGATGATGATGATGATGATGATGATGAT 2146
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QY 2767 AACATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2826
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QY 2887 AAAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2946
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QY 3067 TATTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3113
Db 3184 TATTTTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3230

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RESULT 2

US-08-038-760-2/c
Sequence 2, Application US/08038760
Patent No. 5496731

GENERAL INFORMATION:

APPLICANT: Xu, Hong-Ji
APPLICANT: Hu, Shi-Xue
APPLICANT: Benedict, William F
TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and

```

TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDICIN TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Format to Postscript 4.0, Version #1.05
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08-038-760
FILING DATE: 19930325
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 865-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
US-08-038-760-2
Query Match 99.8% score 3105.4; DB 1; Length 3232
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3106, Conservative 0, Mismatches 1, Indels 0, Gaps 0;
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Db 3113 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 3054
QY 67 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126
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Db 2954 GATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2924
QY 187 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 246
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QY 247 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 306
Db 2874 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2814
QY 247 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 366
Db 2814 AATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2754
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 16, 2003, 23:41:58, Search time 250.854 seconds

(without alignments)
7011.280 Million cell updates/sec

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Perfect score: 4017

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Searched: 2185239 seqs, 115999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

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Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match	Length	DB ID	ALIGNMENTS	Description
1	4017	100.0	2994	11	AA04713	Cancer suppressing
2	4017	100.0	2994	14	AA041545	Retinoblastoma gene
3	4017	100.0	2994	19	AA040064	Retinoblastoma gene
4	4017	100.0	2994	21	AA040287	W13 type human re
5	4017	100.0	2994	20	AA040350	Human p110-RB ret
6	4017	100.0	2994	20	AA040350	cDNA encoding a re
7	4017	100.0	2994	22	AA040350	Retinoblastoma tum
8	4017	100.0	2994	22	AA040350	Retinoblastoma tum
9	4017	100.0	2994	23	AA040350	Retinoblastoma tum
10	4017	100.0	3218	19	AA040350	Modified retinobla
11	4017	100.0	3218	19	AA040350	Sequence of th
12	4017	100.0	3233	15	AA072690	Retinoblastoma 94K
13	4017	100.0	3266	19	AA072690	Modified retinobla
14	4017	100.0	3323	19	AA072690	Modified retinobla
15	4017	100.0	3323	19	AA072690	Modified retinobla
16	4017	100.0	3323	19	AA072690	Modified retinobla
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40	4017	100.0	3554	19	AA072690	Modified retinobla
41	4017	100.0	3554	19	AA072690	Modified retinobla
42	4017	100.0	3554	19	AA072690	Modified retinobla
43	4017	100.0	3554	19	AA072690	Modified retinobla
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45	4017	100.0	3554	19	AA072690	Modified retinobla

Result No.	Score	Match	Length	DB ID	ALIGNMENTS	Description
1	4017	100.0	2994	11	AA04713	Cancer suppressing
2	4017	100.0	2994	14	AA041545	Retinoblastoma gene
3	4017	100.0	2994	19	AA040064	Retinoblastoma gene
4	4017	100.0	2994	21	AA040287	W13 type human re
5	4017	100.0	2994	20	AA040350	Human p110-RB ret
6	4017	100.0	2994	20	AA040350	cDNA encoding a re
7	4017	100.0	2994	22	AA040350	Retinoblastoma tum
8	4017	100.0	2994	22	AA040350	Retinoblastoma tum
9	4017	100.0	2994	23	AA040350	Retinoblastoma tum
10	4017	100.0	3218	19	AA040350	Modified retinobla
11	4017	100.0	3218	19	AA040350	Sequence of th
12	4017	100.0	3233	15	AA072690	Retinoblastoma 94K
13	4017	100.0	3266	19	AA072690	Modified retinobla
14	4017	100.0	3323	19	AA072690	Modified retinobla
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22	4017	100.0	3554	19	AA072690	Modified retinobla
23	4017	100.0	3554	19	AA072690	Modified retinobla
24	4017	100.0	3554	19	AA072690	Modified retinobla
25	4017	100.0	3554	19	AA072690	Modified retinobla
26	4017	100.0	3554	19	AA072690	Modified retinobla
27	4017	100.0	3554	19	AA072690	Modified retinobla
28	4017	100.0	3554	19	AA072690	Modified retinobla
29	4017	100.0	3554	19	AA072690	Modified retinobla
30	4017	100.0	3554	19	AA072690	Modified retinobla
31	4017	100.0	3554	19	AA072690	Modified retinobla
32	4017	100.0	3554	19	AA072690	Modified retinobla
33	4017	100.0	3554	19	AA072690	Modified retinobla
34	4017	100.0	3554	19	AA072690	Modified retinobla
35	4017	100.0	3554	19	AA072690	Modified retinobla
36	4017	100.0	3554	19	AA072690	Modified retinobla
37	4017	100.0	3554	19	AA072690	Modified retinobla
38	4017	100.0	3554	19	AA072690	Modified retinobla
39	4017	100.0	3554	19	AA072690	Modified retinobla
40	4017	100.0	3554	19	AA072690	Modified retinobla
41	4017	100.0	3554	19	AA072690	Modified retinobla
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44	4017	100.0	3554	19	AA072690	Modified retinobla
45	4017	100.0	3554	19	AA072690	Modified retinobla

Result No.	Score	Match	Length	DB ID	ALIGNMENTS	Description
1	4017	100.0	2994	11	AA04713	Cancer suppressing
2	4017	100.0	2994	14	AA041545	Retinoblastoma gene
3	4017	100.0	2994	19	AA040064	Retinoblastoma gene
4	4017	100.0	2994	21	AA040287	W13 type human re
5	4017	100.0	2994	20	AA040350	Human p110-RB ret
6	4017	100.0	2994	20	AA040350	cDNA encoding a re
7	4017	100.0	2994	22	AA040350	Retinoblastoma tum
8	4017	100.0	2994	22	AA040350	Retinoblastoma tum
9	4017	100.0	2994	23	AA040350	Retinoblastoma tum
10	4017	100.0	3218	19	AA040350	Modified retinobla
11	4017	100.0	3218	19	AA040350	Sequence of th
12	4017	100.0	3233	15	AA072690	Retinoblastoma 94K
13	4017	100.0	3266	19	AA072690	Modified retinobla
14	4017	100.0	3323	19	AA072690	Modified retinobla
15	4017	100.0	3323	19	AA072690	Modified retinobla
16	4017	100.0	3323	19	AA072690	Modified retinobla
17	4017	100.0	3455	19	AA072690	Modified retinobla
18	4017	100.0	3455	19	AA072690	Modified retinobla
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38	4017	100.0	3554	19	AA072690	Modified retinobla
39	4017	100.0	3554	19	AA072690	Modified retinobla
40	4017	100.0	3554	19	AA072690	Modified retinobla
41	4017	100.0	3554	19	AA072690	Modified retinobla
42	4017	100.0	3554	19	AA072690	Modified retinobla
43	4017	100.0	3554	19	AA072690	Modified retinobla
44	4017	100.0	3554	19	AA072690	Modified retinobla
45	4017	100.0	3554	19	AA072690	Modified retinobla

XX W09005180-A.
 XX 17-MAY-1990.
 XX 30-OCT-1989: 89WC-0004808.
 XX 31-OCT-1988: 88US-0265829.
 XX (REGC) UNIV OF CALIFORNIA.
 XX Lee WH, Huang HJS:
 XX WPI: 1990-178822/23.
 XX P-PSDB: AAR05305.
 XX Controlling cancer
 XX by replacing ineffective cancer suppressing gene with cloned.
 XX active gene.
 XX Claim 35: Page 86, 105pp; English.
 XX Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA.
 XX By installing a working CGS, safe and specific treatment and
 XX prophylaxis can be given to cancer patients.
 XX Sequence 2994 BP: 974 A; 618 C; 593 G; 809 T; 0 other:
 Alignment Scores:
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 Score: 4017.00 Matches: 761
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
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 QY 21 ThrGlyGluLeuLeuLysTyrLeuThrGlnProSerSerLysSerThrGlnLeuAsnSer 40
 DB 640 ACAATGACTATATATTGACACACACGACAGTTGATCTATCTGATCAATTAATTTCT 699
 QY 41 AlaLeuValLeuLysValSerTyrPheThrPheLeuLeuAlaLysGlyLeuValLeuGln 60
 DB 700 GCATTCGTGCTAAAGCTTCTGACATCACAATTTATAGCTAAAGCGGAGATTTACAA 759
 QY 61 MetGluAspLeuValLysSerPheGlnLeuMetLeuLysValLeuAspTyrPheLeu 80
 DB 760 ATGCAAAATGCTGCTGATTTATTTTCAATGATGATGATGATGATGATGATGATGAT 819
 QY 81 LysLeuSerProPheMetLeuLeuLysGlnProTyrLysThrAlaValLeuProLysLeu 100
 DB 820 AAATCTCACTCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 879
 QY 161 GlySerProArgThrProAlaGlyGlyGlnAsnArgSerAlaArgLeuAlaLysLeu 120
 DB 880 GGTTCACCTGACACACCCAGCCAGGAGGACAGACAGAGAGAGAGAGAGAGAGAGAGAG 939
 QY 121 GluAsnAspThrAlaGlyLeuValLeuLysGlnLysGlnLysGlnLysGlnLysGln 140
 DB 940 GAAATATATCAAGATATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 999
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 QY 161 SerAsnGlyLeuProGlnValGluAsnLeuSerLysArgTyrGlnGlnLeuLysLeu 180
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 QY 201 PheAspSerPheGlnThrGlnLeuThrGlnAlaGlySerAsnLeuAspGlnValAsn 220
 DB 1180 ATGACACTTTTCAACACACAGACACACACACACACACACACACACACACACACACACAC 1239
 QY 221 ValLeuProGlnLysThrProValAlaGlnValMetAsnThrLysGlnLeuMetMet 240
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 QY 241 LeuLysAsnSerLysSerAspThrProSerGlnLysLeuLysLeuSerTyrPheAsnAsnGly 260
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 QY 321 LeuSerLysGlnAsnProLysLeuLeuAspAspAsnLeuPheGlnSerLysLeuGln 340
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 QY 341 AlaGlyAlaLeuGlnValAlaValMetAlaThrTyrSerAlaGlySerThrSerGlnLeuAsp 360
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 DB 1780 AAACATTTTAC 1839
 QY 421 ProLeuPheAspLeuLeuLysGlnSerLysAspArgGlyGlyProThrAspHisLeuGln 440
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 QY 441 SerAlaGlyProLysAsnLeuProLeuGlnLysAsnHisThrAlaAlaAspMetTyrLeu 460
 DB 1900 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1959
 QY 461 SerProValArgSerProLysGlnLysGlnSerThrThrValAlaGlnSerThrAlaAsn 480
 DB 1960 TCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2019
 QY 481 AlaLeuThrGlnAlaThrSerAlaPheSerThrGlnLysProLeuLysSerThrSerLeu 500
 DB 2020 TCTGCAAAATGCTGATTTTCAAAATTTTATATCTTTATGATGATGATGATGATGAT 2079
 QY 501 SerLeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgGlnAsnProLeuGlnGln 520
 DB 2080 TCACTGTTTATTAATAAAATGCTATGCTATGCTATGCTATGCTATGCTATGCTATGCTATG 2139
 QY 521 ArgLeuLeuSerGlnHisProGlnGlnLysLeuLysLeuLysLeuLysLeuLysLeuLys 540
 DB 2140 CCGCTTCTGCTGAC 2199

QY	541	LeuGlnAsnGluTyr-GluLeuMetArgAspArgHisLeuAspGlnIleMetMetCysSer	560
Db	2200	CTCCAGCAATGAGATGATGAACTCATATGAGAGACAGGCAATTGGACCAAAATTATGATGGTGTCC	2259
QY	561	MetTyrGlyIleCysValValysAsnIleAspLeuysPheLysIleIleValThrAla	580
Db	2260	ATCTATGCGATATGCAAACTGCAAGCAATATACACTTAAATTCAAAATTCATTATTAACAGCA	2319
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Db	2320	TACAGAGATCTTCCTCATCTCTTCCTGGAGACATTCAAAAGTGTGTGATCAAGAGACAG	2379
QY	601	GluTyrAspSerIleIleValPheTyrAsnSerValPheMetGlnArgLeuysThrAsn	620
Db	2380	GAGATATCTCTATTATAGATTCTATAAATCGGCTTCATGCGAGACGAGACGAAAACAAAT	2439
QY	621	IleLeuGlnTyrAlaSerThrArgProProthrlleuSerProIleProHisIleProCys	640
Db	2440	ATTGTGACGATAGCTTTCACACAGCCCCCTACTCTGTGTACCAATACCTCATCTCCTCGCA	2499
QY	641	SerProTyrLysPheProSerSerProLeuArgIleProGlyIleAsnIleTyrIleSer	660
Db	2500	AGCCTTACAGATTCTCTATTTACCTTACCCCTTACGCAATTCCTGAGAGAAATCTATATTTC	2559
QY	661	ProLeuLysSerProTyrLysIleSerGlnGlyLeuProThrProThrLysMetThrPro	680
Db	2560	CCCCGAGAGATGCATATTAATAATTTCCAGAGGCTGTCCCAACCAACCAAAATGATCCCA	2619
QY	681	ArgSerArgIleLeuValSerIleGlyGluSerPheGlyThrSerGlnLysPheGlnLys	700
Db	2620	AGATCAGAGATCTTAGTATCATGTGAGATCATTCGCGACATTCAGAAATTCACAGAAA	2679
QY	701	IleAsnGlnMetValCysAsnSerAspArgValleuLysArgSerAlaGlnGlySerAsn	720
Db	2680	ATTAATCATATGATGATGTAAACAGGACCGCTGTCTCAAAAAGATGCTGAGAGAAAGAAC	2739
QY	721	ProProLysProLeuLysLysLysLeuArgPheAspIleGlnGlySerAspGlnAlaAspIy	740
Db	2740	CCCTCTAAACCACTGAAAAAAGCTTGCATATTTGATTCAGAGATCATAGACAGATGCA	2799
QY	741	SerTyrHisLeuProGlyLysLeuSerLysPheGlnGlnLysLeuAlaGluMetThrSerThr	760
Db	2800	AGTAAACATCTCCACAGACATCCAAATTTACAGAGAAATCGCCAGCAAAATGACTCTTACT	2859
QY	761	ArgThrArgMetGlnLysGlnLysMetLysAspSerMetLysPheSerAsnLysGlnGlu	780
Db	2860	CGAACACAGATGCAAAAAGCAAAATGATATAGCATGATATCTTCAAAACAGAGAGAG	2919
QY	781	Lys 781	
Db	2920	AAA 2922	
RESULT 2			
AAQ41545			
ID AAQ41545 standard, DNA: 2994 bp.			
AC XX			
AT XX			
CT XX			
DE 24-AUG-1993 (first entry)			
XX XX			
DE Metnoblstroma gene.			
XX XX			
FH RB gene product: p56RB portion; cell cycle progression control;			
FH RB combination: therapeutic methods; arrest; tumorigenesis;			
FH KM regulation; physiological processes; blood cell prodn.;			
FH KM gamete prodn.; ss.			
OS XX			
OS Homo sapiens SR-40 cell line.			
FH Key location/Qualifiers			
FH FT 139..2925			
FH CDS /tag= a			
FH FT /note= "Rb protein"			

[illegible]

GenCore version 5.1.3
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 18, 2003, 04:12:19 ; Search time 44.4279 seconds

(Without alignments)
5391.080 Million cell updates/sec

Title: US-09-026-459A-37

Perfect score: 4017

Sequence: 1 MSRLKXVDLFALEFKLEP

Scoring table: BLOSUM62

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Ygapop	10.0	Ygapext	0.5
Dgapop	6.0	Dgapext	7.0
Delop	6.0	Delext	7.0

Searched: 441362 seqs, 153338361 residues

Total number of hits satisfying chosen parameters: 862724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 100%

Listing first 45 summaries

Command line parameters:
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-DB=Issued_Patents_NA -QFMT=fastap -SUFF=ini -MINMATCH=0 -1 -LOOPTCL=0
-LOOPTCL=0 -PNTS-bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR_SCORE=100 -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
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Database:

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6: /cgnt2_6/ptodata/1/ina/Backfiles.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	4017	100.0	2994	1	US-08-204-329-2	Sequence 2, Appl.
2	4017	100.0	2994	2	US-08-482-627-4	Sequence 4, Appl.
3	4017	100.0	2994	4	US-08-801-092-3	Sequence 3, Appl.
4	4017	100.0	2994	4	US-09-315-113-3	Sequence 3, Appl.
5	4017	100.0	2995	4	US-08-359-648-7	Sequence 7, Appl.
6	4017	100.0	3232	1	US-08-038-760-1	Sequence 1, Appl.
7	4017	100.0	3232	1	US-08-038-760-2	Sequence 1, Appl.
8	4017	100.0	3232	2	US-08-470-091-1	Sequence 2, Appl.
9	4017	100.0	3232	2	US-08-470-091-2	Sequence 2, Appl.
10	4014	99.9	2994	5	PCT-US94-10357-1	Sequence 1, Appl.
11	4007	99.8	2995	4	US-08-328-673A-7	Sequence 7, Appl.
12	768	19.1	2808	1	US-07-708-962-1	Sequence 1, Appl.

Result No.	Score	Match	Length	DB	ID	Description
13	763	19.0	2808	2	US-08-153-721D-1	Sequence 1, Appl.
14	729.5	18.2	4853	1	US-08-833-883-1	Sequence 1, Appl.
15	729.5	18.2	4853	2	US-08-833-883-1	Sequence 1, Appl.
16	727.5	18.1	3249	1	US-08-106-493A-1	Sequence 1, Appl.
17	727.5	18.1	3249	1	US-08-123-264-1	Sequence 1, Appl.
18	516.5	12.4	3747	4	US-09-211-253D-2	Sequence 2, Appl.
19	144	3.6	6773	4	US-09-166-360-27	Sequence 27, Appl.
20	143.5	3.6	3763	1	US-07-762-665D-1	Sequence 1, Appl.
21	143	3.6	3593	4	US-09-404-627-3	Sequence 3, Appl.
22	140	3.5	4205	4	US-09-404-627-1	Sequence 1, Appl.
23	140	3.5	8789	1	US-08-328-254-5	Sequence 5, Appl.
24	138	3.4	3883	1	US-08-468-036-33	Sequence 33, Appl.
25	138	3.4	3883	2	US-08-468-036-33	Sequence 33, Appl.
26	138	3.4	3884	4	US-09-541-782-3	Sequence 3, Appl.
27	138	3.4	4868	4	US-09-723-820-3	Sequence 3, Appl.
28	138	3.4	4868	4	US-08-139-937-12	Sequence 12, Appl.
29	136	3.4	4868	5	PCT-US94-16100-12	Sequence 12, Appl.
30	137	3.4	10136	5	PCT-US94-16100-12	Sequence 12, Appl.
31	137	3.4	10136	5	PCT-US94-16100-12	Sequence 12, Appl.
32	131	3.3	2415	4	US-09-134-001C-2381	Sequence 2381, Appl.
33	130	3.2	5893	2	US-08-487-080-44	Sequence 44, Appl.
34	130	3.2	5893	2	US-08-487-080-44	Sequence 44, Appl.
35	127.5	3.2	5181	1	US-08-257-073-10	Sequence 10, Appl.
36	126	3.2	10254	4	US-08-961-522-29	Sequence 29, Appl.
37	121	3.0	6152	4	US-08-973-452-2	Sequence 2, Appl.
38	121	3.0	6152	4	US-08-973-452-2	Sequence 2, Appl.
39	119	3.0	10546	4	US-09-134-001C-322	Sequence 322, Appl.
40	118.5	2.9	3492	4	US-08-923-992A-9	Sequence 9, Appl.
41	117.5	2.9	7493	1	US-08-212-133A-7	Sequence 7, Appl.
42	117.5	2.9	7493	1	US-08-474-603-5	Sequence 5, Appl.
43	117.5	2.9	7493	2	US-08-670-707A-5	Sequence 5, Appl.
44	117.5	2.9	7493	2	US-09-037-601-5	Sequence 5, Appl.
45	117.5	2.9	7493	4	US-09-315-179-5	Sequence 5, Appl.

ALIGNMENTS

Result 1
Sequence 2, Application US/06204329
Patent No. 5710255
GENERAL INFORMATION:
APPLICANT: SHEPARD, H. M.
APPLICANT: MEN, SHU F.
TITLE OF INVENTION: CHARACTERIZATION OF A NOVEL ANTI-P110RB
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,329
FILING DATE: 15-AUG-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05886
FILING DATE: 14-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: RENE A. FITTS
REGISTRATION NUMBER: 35,136
REFERENCE/BOOKER NUMBER: 16940-00040005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422

```

1 INFORMATION FOR SEQ ID NO: 2
2
3 SEQUENCE CHARACTERISTICS:
4
5     LENGTH: 2994 base pairs
6
7     TYPE: nucleic acid
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9     STRANDEDNESS: double
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11     TOPOLOGY: linear
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13     MOLECULE TYPE: DNA (cdna)
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Alignment Scores:
Prod No.:

Pred. NO.:	0	length:	2994
Score:	4017.00	Matches:	781
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
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$$(4667.1) \quad 3.675 \pm 07.40 \text{ g} \times (187.1) \quad 1) - V_{\text{eff}} = 470.60 - 50$$

579 1 MetSerArgyleuleuLysLysIAspValIleuPheIleuPheSerLysIleuGluArg 20
 580 ATGTCAAGACTGTTGAAGACGATGATGTTGTTGCACCTCTGACCAAAATTCGAAAC 633

67 21 ThrGsgIuDeuIeYrLeuThgImProSerSerIleSerThgIuIeAsnSer 40
 |||
 640 ACATGTGAACCTATATATTGACCAACACAGCAGCTTCGATATCTGAAATAAATT 699

CY 41 AAlaIeuValIeuLysValSerTTrPIeThrPheLeuLeuAlaLysCylGluValIeuGln 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 700 GCATGGTGCTAAAGTTTCITGGATCCATTTTATTACGTAAAGCGAAGATTACAA 75

QY 61 MetGluAspSpleuValIieserPhegInLeuNelLeucysValLeuAspTyrrheile 80
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 Db 760 ATGAGATGATCTGTGATTCATTTCAAGTTATGCTATGCTGCTGACATTATT 81

Dy 81 LysLeuSerProFroMetLeuLeuLysGluProTyrIleThrAlaValIleProIleAsn 100
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Db 820 AAcTCACCTCCCAATGTACTCAAGAACCATATAAAAGAAGCTGTATTACCCTAAT 87

Qy 101 GlySerProArgThrProArgArgGlycylAsnArgSerAlaArgIleAlaLysGlnLeu 120
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QY 121 GluSnAspThrArgIleIleValLeuCysLysGluHisGluCysAsnIleAspGlu 140
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IDB 940 GAAAGACATACAGAAATATGAGACTCTCTCTAAGAGAAATGATATGATATGATAGAC 999

cy 141 ValLysAsnValTyrPheLysAsnPheIleProPheMetLysSerLeuGlyLeuValThr 160
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D_b 106C CTATGACCTCCAGAGGTGAATAATTCTTCTTAACGGATACGAGAATAATTATCTTAA 117

O_y 161 SerSrnGlyLeuProGluValGluAsnLeuSerLysArgTyrGlnIleIeYrLeuLys 180

QY 181 AsnLysAspLeuAspAlaArgLeuPheLeuAspHisAspLysThrLeuGlnThrAspSer 200
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201 IleaspsrfeeglufrglnarqThfProArqySSerAsnLeuaspglucluvaiAsn 220

Oy	221	VallieProHISThrProValArgThrValMetAsnIleGlnGluMetCys	240
Ch	1248	GATTCTTAAAGATTTAATAATTAACCAACTGGTCCTTGCCCGGTGA	1267

[illegible]

261 ThrValAsnProLysGluSerIleLeuLysArgValLysAspIleGlyTyrIlePheLys 280

1360 ACAGTGAATCTAAAGTAAGTATATCTGAAAA-NTTGAAGATATTCATATACATCTTTTAA 1419

[illegible]

a7 | aaglyValAlaLeuTyrPheArgValMetGlnGluCysMetThrLysSerProTyrGlnArg 820
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b6 |-----
1480 CTGGAGTCCTGCCATTATACCGAGCAATGCATCATGTTAAATCGAACACAAGAACGA 1539

Cy	121	LESCSRLleGlnasrPheSerLysIcoulouasnAspAsn[Le]hoHisMetSerLeucou	340
Dd	1540	TATTCATTCCAAATTTAGAAGTCTGTGAAGAACAATTTCAATACGTCTTAITS	1596

341 AAdGysAlAdeUcUuaValMetAlaThrTrpSerArgSerIleSerClnAsnLeuasp 360
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1600 GGTGGCGCTTTCACCTTTTGATGGCAATAAGACAACTAACACTCATCTTCA 165

361 SerGlyThrAspLeuSerPheProTrpIleLeuAsnValIleAsnLysAlaPheAsp 380
 1650 TCAGCAACGATTTGTCTTTGCCCATGATCTTCGATCTGCTTAATTTAAAGGCTTCAAT 1719

67 PheylrlygValllleclusePheellhelypaladlasyasloulllrArgqlMetllle 400
120 TTTACCAAGTGAATCAAAGCTTTTAAAGAGAGAGCGATTAAAGGAGGATATAA 177

401 LYSIHSLEQDIATGCGYSGLHISARGILEMCTGUSERIEALIPPIVDSRASPQR 420
 1740 AAGCATATGACAGCATCTTCACATCATCATTCATGACATCCCTGCATATGATGCAATCA 1839

QY 421 ProLeuPheAspLeuIleLysGlnSerLysAspArgIuGlyProThrAspHisLeuGln 440
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 DB 1840 CCTTATTTCATCTTATTAAACAATCAAGACACCGGAAGAGCCCAACGATCAGCTGAA 1899

QY 441 SOTAACCTPGLDASNLGFTGLGGTAAAGSASHISTHAIADASPMTPTTGG 460
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Db 1906 TGAATTAATTGTATTTCTTGCAATAATTCATATGACCAATATGATCTT 1929
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QY 461 SerProValArgSerProIysIysIysClySerThrThrArgValAsnSerThrAlaAsn 480
|||||
DB 1960 TCCCTGTAAGATTCGCAAGAAAGAGCGTCGCAAGCGGCTAAATGCTACGGCAAA 2010

QY 481 AlaGluThrGlnAlaThrSerAlaPheGlnThrGlnIysProLeuIysSerThrSerArg 500
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db 2020 GACAGAACCAAGCAAGCTCCAGCCTCCAGACCGTAAAGGCCCTTCGAATCTGGCTGTCTTT 5076

607 SerLeuPheTyrIleGlyValIleTyrArgLeuAlaIleTyrLeuArgGluAsnThrLeuCysSer 520
608 TACTGGTTATATAAAAGCTATTGGCTAAGCTATTCCTACCAAGCCTATCTATTAAGG
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[illegible]

541 English Literature, Melville, Ralph Waldo Emerson, Hawthorne, Melville, Poe, Whitman, American Literature, American Studies, American History, American Culture, American Society, American Politics, American Economics, American Geography, American Science, American Technology, American Art, American Music, American Film, American Theater, American Literature, American Studies, American History, American Culture, American Society, American Politics, American Economics, American Geography, American Science, American Technology, American Art, American Music, American Film, American Theater

[illegible]

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581 PyTysaspIcHrOHSAlAvalGInclOthrPhelysArgValLeuIleGlySerC670
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601 GlnTyrAspSerIleIleValPheCysArgGlnValAlaPheMetGluArgLeuLysHisAsn 620

DG 2580 GAGATGATTCATTAAAGTAACTTAACCGGTCTCATGCAGAGAGTGCAACAACAAT 2639

O7 621 Ttctcgtintyytaaserthayfrprcthmiaeserproifecthonisierptary 640

[illegible]